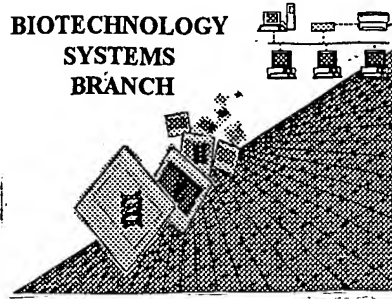# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/023,066_
Source: _OIPE_
Date Processed by STIC: _1/15/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
            Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, r other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

<u>ERROR DETECTED</u>   <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: *10/023066*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
       Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3 _____ Misaligned Amino
       Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; **use space characters, instead.**

4 _____ Non-ASCII

The submitted file was **not saved in ASCII(DOS) text, as required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
       "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____ . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences
       (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each skipped sequence:**
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
       (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
       (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
       Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial-Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
       "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single **nucleotide** in a nucleic acid sequence. N is **not** used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING   DATE: 01/15/2002
PATENT APPLICATION: US/10/023,066   TIME: 19:01:05

    Input Set : A:\BB1037 Sequence Listing.txt
    Output Set: N:\CRF3\01152002\J023066.raw

            SEQUENCE LISTING
  3 (1) GENERAL INFORMATION:
  5   (i) APPLICANT: E. I. DU PONT DE NEMOURS AND
  6   COMPANY
  8   (ii) TITLE OF INVENTION: CHIMERIC GENES AND
  9   METHODS FOR INCREASING
 10   *delete →* ~~INCREASING~~ THE LYSINE
 11   *duplicate* AND THREONINE CONTENT
W--> 12   **OF THE SEEDS OF PLANTS**
 14   (iii) NUMBER OF SEQUENCES: 107
 16   (iv) CORRESPONDENCE ADDRESS:
 17   (A) ADDRESSEE: E. I. DU PONT DE NEMOURS
 18   AND COMPANY
 19   (B) STREET: 1007 MARKET STREET
 20   (C) CITY: WILMINGTON
 21   (D) STATE: DELAWARE
 22   (E) COUNTRY: U.S.A.
 23   (F) ZIP: 19898
 25   (v) COMPUTER READABLE FORM:
 26   (A) MEDIUM TYPE: FLOPPY DISK
 27   (B) COMPUTER: IBM PC COMPATIBLE
 28   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 29   (D) SOFTWARE: MICROSOFT WORD VERSION 2.0C
 31   (vi) CURRENT APPLICATION DATA:
 32   **(A) APPLICATION NUMBER: US/10/023,066**
 33   **(B) FILING DATE: 17-Dec-2001**
 34   (C) CLASSIFICATION:
 36   (viii) ATTORNEY/AGENT INFORMATION:
 37   (A) NAME: BARBARA C. SIEGELL
 38   (B) REGISTRATION NUMBER: 30,684
 39   (C) REFERENCE/DOCKET NUMBER: BB-1037-C
 41   (ix) TELECOMMUNICATION INFORMATION:
 42   (A) TELEPHONE: 302-992-4931
 43   (B) TELEFAX: 302-773-0164
 44   (C) TELEX: 835420

ERRORED SEQUENCES

234 (2) INFORMATION FOR SEQ ID NO: 6:
236   (i) SEQUENCE CHARACTERISTICS:
237   (A) LENGTH: 917 base pairs
238   (B) TYPE: nucleic acid
239   (C) STRANDEDNESS: single
240   (D) TOPOLOGY: linear
242   (ii) MOLECULE TYPE: DNA (genomic)
244   (ix) FEATURE:

pp 1, 3-4

Does Not Comply
Corrected Diskette Needed
(please try to lengthen each line - thus, fewer lines will be shown)

p. 3

Input Set : A:\BB1037 Sequence Listing.txt
Output Set: N:\CRF3\01152002\J023066.raw

```
245           (A) NAME/KEY: CDS
246           (B) LOCATION: 3..911
248   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
250 CC ATG GCT ACA GGT TTA ACA GCT AAG ACC GGA GTA GAG CAC TTC GGC    47
251    Met Ala Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly
252     1           5                  10                  15
254 ACC GTT GGA GTA GCA ATG GTT ACT CCA TTC ACG GAA TCC GGA GAC ATC    95
255 Thr Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile
256                 20                  25                  30
258 GAT ATC GCT GCT GGC CGC GAA GTC GCG GCT TAT TTG GTT GAT AAG GGC   143
259 Asp Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly
260             35                  40                  45
262 TTG GAT TCT TTG GTT CTC GCG GGC ACC ACT GGT GAA TCC CCA ACG ACA   191
263 Leu Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr
264          50                  55                  60
266 ACC GCC GCT GAA AAA CTA GAA CTG CTC AAG GCC GTT CGT GAG GAA GTT   239
267 Thr Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val
268       65                  70                  75
270 GGG GAT CGG GCG AAG CTC ATC GCC GGT GTC GGA ACC AAC AAC ACG CGG   287
271 Gly Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg
272 80                  85                  90                  95
274 ACA TCT GTG GAA CTT GCG GAA GCT GCT GCT TCT GCT GGC GCA GAC GGC   335
275 Thr Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly
276                100                 105                 110
278 CTT TTA GTT GTA ACT CCT TAT TAC TCC AAG CCG AGC CAA GAG GGA TTG   383
279 Leu Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu
280             115                 120                 125
282 CTG GCG CAC TTC GGT GCA ATT GCT GCA GCA ACA GAG GTT CCA ATT TGT   431
283 Leu Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys
284          130                 135                 140
286 CTC TAT GAC ATT CCT GGT CGG TCA GGT ATT CCA ATT GAG TCT GAT ACC   479
287 Leu Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr
288       145                 150                 155
290 ATG AGA CGC CTG AGT GAA TTA CCT ACG ATT TTG GCG GTC AAG GAC GCC   527
291 Met Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala
292 160                 165                 170                 175
294 AAG GGT GAC CTC GTT GCA GCC ACG TCA TTG ATC AAA GAA ACG GGA CTT   575
295 Lys Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu
296                 180                 185                 190
298 GCC TGG TAT TCA GGC GAT GAC CCA CTA AAC CTT GTT TGG CTT GCT TTG   623
299 Ala Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu
300             195                 200                 205
302 GGC GGA TCA GGT TTC ATT TCC GTA ATT GGA CAT GCA GCC CCC ACA GCA   671
303 Gly Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala
304          210                 215                 220
306 TTA CGT GAG TTG TAC ACA AGC TTC GAG GAA GGC GAC CTC GTC CGT GCG   719
307 Leu Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala
308       225                 230                 235
310 CGG GAA ATC AAC GCC AAA CTA TCA CCG CTG GTA GCT GCC CAA GGT CGC   767
```

Input Set : A:\BB1037 Sequence Listing.txt
Output Set: N:\CRF3\01152002\J023066.raw

```
 311 Arg Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg
 312 240             245             250             255
 314 TTG GGT GGA GTC AGC TTG GCA AAA GCT GCT CTG CGT CTG CAG GGC ATC    815
 315 Leu Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile
 316             260             265             270
 318 AAC GTA GGA GAT CCT CGA CTT CCA ATT ATG GCT CCA AAT GAG CAG GAA    863
 319 Asn Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu
 320             275             280             285
E--> 322 CTT GAG GCT CTC CGA GAA GAC ATG AAA AAA GCT GGA GTT CTA TAA TGAGAATTC (918) 917
 323 Leu Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu  *
 324             290             295             300
1741 (2) INFORMATION FOR SEQ ID NO: 67:
1743     (i) SEQUENCE CHARACTERISTICS:
1744         (A) LENGTH: 28 amino acids
1745         (B) TYPE: amino acid
1746         (C) STRANDEDNESS: unknown
1747         (D) TOPOLOGY: unknown
1749    (ii) MOLECULE TYPE: protein
1751    (ix) FEATURE:
1752         (A) NAME/KEY: Protein
1753         (B) LOCATION: 1..28
1754         (D) OTHER INFORMATION: /label= name
1755 /note= "(SSP 5)4"
1757    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:
1759 Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
1760 1           5               10              15
1762 Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
E--> 1763             20               25
1980 (2) INFORMATION FOR SEQ ID NO: 76:
1982     (i) SEQUENCE CHARACTERISTICS:
1983         (A) LENGTH: 175 base pairs
1984         (B) TYPE: nucleic acid
1985         (C) STRANDEDNESS: double
1986         (D) TOPOLOGY: linear
1988    (ii) MOLECULE TYPE: DNA (genomic)
1990    (vi) ORIGINAL SOURCE:
1991         (B) STRAIN: E. coli
1992         (G) CELL TYPE: DH5 alpha
1994   (vii) IMMEDIATE SOURCE:
1995         (B) CLONE: 5-1
1997    (ix) FEATURE:
1998         (A) NAME/KEY: CDS
1999         (B) LOCATION: 2..172
2000         (D) OTHER INFORMATION: /function= "synthetic
2001 storage protein
2002 /product= "protein"
2003 /gene= "ssp"
2004 /standard_name=
2005 "5.5.5.7.7.7.7.5"
```

[handwritten annotations: "20", "25", "misaligned amino acid number (see item 3 on Error Summary Sheet)", "p.4"]

Input Set : A:\BB1037 Sequence Listing.txt
Output Set: N:\CRF3\01152002\J023066.raw

```
2007     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:
2009 C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG     46
2010   Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
2011    1                 5                 10                15
2013 GAG GAG AAG ATG AAG GCG ATG GAG GAA AAG CTG AAA GCG ATG GAG GAG  94
2014 Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
2015                   20                  25                30
2017 AAA CTC AAG GCT ATG GAA GAA AAG CTT AAA GCG ATG GAG GAG AAA CTG 142
2018 Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu
2019                 35                  40                  45
E--> 2021 AAG GCC ATG GAA GAG AAG ATG AAG GCG TGATAG
2022 Lys Ala Met Glu Glu Lys Met Lys Ala
2023            50              55
2515 (2) INFORMATION FOR SEQ ID NO: 98:
2517      (i) SEQUENCE CHARACTERISTICS:
2518          (A) LENGTH: 59 base pairs
2519          (B) TYPE: nucleic acid
2520          (C) STRANDEDNESS: single
2521          (D) TOPOLOGY: linear
2523     (ii) MOLECULE TYPE: DNA (genomic)
2525     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:
E--> 2527 CATGGCGCCC ACCGTGATGA TGGCCTCGTC GGCCACCGCC GTCGCTCCGT TCCAGGGGC
W--> 2528 59
2530 (2) INFORMATION FOR SEQ ID NO: 99:
2532      (i) SEQUENCE CHARACTERISTICS:
2533          (A) LENGTH: 59 base pairs
2534          (B) TYPE: nucleic acid
2535          (C) STRANDEDNESS: single
2536          (D) TOPOLOGY: linear
2538     (ii) MOLECULE TYPE: DNA (genomic)
2540     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:
E--> 2542 TTAAGCCCCT GGAACGGAGC GACGGCGGTG GCCGACGAGG CCATCATCAC GGTGGGCGC
W--> 2543 59
2700 (2) INFORMATION FOR SEQ ID NO: 107:
2702      (i) SEQUENCE CHARACTERISTICS:
2703          (A) LENGTH: 29 base pairs
2704          (B) TYPE: nucleic acid
2705          (C) STRANDEDNESS: single
2706          (D) TOPOLOGY: linear
2708     (ii) MOLECULE TYPE: DNA (genomic)
2710     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:
2712 CTCTCGGTAC CTAGTACCTA CTGATCAAC                                   29
E--> 2714 BB-1037-C
```

(179) 175

59

see item 1
on Error
Summary Sheet

59

delete

Input Set : **A:\BB1037 Sequence Listing.txt**
Output Set: **N:\CRF3\01152002\J023066.raw**

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:12 M:259 W: Allowed number of lines exceeded, (ii) TITLE OF INVENTION:
L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:322 M:254 E: No. of Bases conflict, Input:918 Counted:917 SEQ:6
L:776 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:843 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:1380 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1763 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:67
L:2021 M:254 E: No. of Bases conflict, Input:179 Counted:175 SEQ:76
L:2527 M:254 E: No. of Bases conflict, Input:0 Counted:59 SEQ:98
L:2528 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:98
L:2542 M:254 E: No. of Bases conflict, Input:0 Counted:59 SEQ:99
L:2543 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:99
L:2638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104
L:2714 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:2714 M:333 E: Wrong sequence grouping, Amino acids not in groups!